and both strands were sequenced using Prism dye-terminator sequencing kits and an ABI 377 sequencing machine. Sequences of human Mabs-derived heavy and kappa chain transcripts were obtained by direct sequencing of PCR products generated from poly(A+) RNA using the primers described above. All sequences were analyzed by alignments to the "V BASE sequence directory" (Tomlinson et al., MRC Centre for Protein Engineering, Cambridge, UK) using MacVector and Geneworks software programs.

IN THE SEQUENCE LISTING:

Please enter the contents of the new substitute paper copy of the sequence listing, filed concurrently herewith, into the specification.

REMARKS

Status of the Claims

Claims 44-51 remain rejected only under 35 USC § 112 first paragraph, all rejections under § 112 second paragraph, § 102 and § 103 having been obviated by the amendment filed January 4, 2002.[1]

Applicants herein cancel claims 44-51 and add claims 52-61 by amendment herein.

Compliance With the Sequence Listing Rules

The specification is objected to under 37 CFR § 1.821(d). Specifically, the Examiner noted that two

[1] Page 3 of the Office Action, underlined statement prior to "Claims Rejections - 35 USC § 112."

sequences disclosed in the specification did not have a SEQ ID NO. associated therewith.

In response, applicants have amended the specification to include a SEQ ID NO. for each sequence and file concurrently herewith a substitute paper copy and a substitute computer readable form copy of the Sequence Listing which contain the sequences, as well as the requisite statement set forth below. Applicants have also requested that the contents of the new substitute paper copy of the sequence listing be entered into the specification. Applicants respectfully submit that the application is now fully compliant with the sequence listing rules under 37 CFR §§ 1.821-1.825.

Statement Regarding the Sequence Listings

The contents of the new substitute paper copy and the new substitute computer readable copy of the sequence listing are the same and neither adds new matter.

Objections to the Drawings

Applicants file concurrently herewith formal drawings that correct the noted informalities. Applicants respectfully submit that all drawings are presently in compliance with 37 CFR § 1.84.

Replacement IDS

The Examiner states the references crossed-out on the Form PTO-1449 were not found in the application. Copies of the references from the original IDS, which applicants have now provided on two prior occasions, are submitted concurrently herewith. Applicants also submit

concurrently herewith a copy of the original IDS and the form PTO-1449 (in duplicate).

Amendments to the Claims

Claims 44-51 stand rejected solely under 35 USC § 112 first paragraph.

In particular, the Examiner cites lack of written description, new matter and enablement as the bases for rejection. Solely for purposes of advancing prosecution, applicants have cancelled claims 44-51 without prejudice, thereby obviating the rejections. Applicants respectfully submit that claims 52-61, newly added by amendment herein, are fully compliant with 35 USC § 112 first paragraph and request an early and favorable action.

New claim 52 is similar to claim 44, now cancelled, in reciting a method of extending the serum half-life of an antibody. However, rather than reciting a first and at least second moiety capable of binding to FcRb receptor (as in claim 44), claim 52 recites a first and at least second IgG region capable of binding to FcRb receptor. As noted by the Examiner, applicants are fully in possession of a genus comprising such IgG regions.[2] Thus, there exists adequate written description for claim 52 and the claims depending therefrom (claims 53-57).

New claim 58 is similar to claim 49, now cancelled, in reciting an antibody with an extended serum half-life. However, rather than reciting a first and at least second moiety capable of binding FcRb receptor, claim 58 recites a first and at least second IgG region capable

[2] Office Action page 4, second full paragraph.

of binding FcRb receptor. As noted above, the Examiner agrees that applicants are in full possession of a genus comprising such IgG regions. Thus, there exists adequate written description for claim 58 and the claims depending therefrom (claims 59 - 61).

The Examiner criticizes the recited pH-dependence. Recitation in the claims of greater avidity of binding at pH 7.4 was erroneous and applicants thank the Examiner for bringing the error to their attention. In the claims newly added by amendment herein, pH-dependence of binding is also recited, but now correctly refers to greater avidity of binding at ***pH 6.0***, not pH 7.4. Thus, the new claims are free of the written description, new matter, and enablement rejections lodged against the formerly pending, now cancelled, claims.

As discussed above, the amendment of the claims to recite a first and at least second IgG region capable of binding FcRb receptor in a pH dependent manner is fully supported by the specification and thus adds no new matter.

New claims 55 and 61 recite a mutated antibody hinge region comprising one less cysteine residue as compared to the corresponding wild type hinge region. Support for this element is found generally throughout the specification and particularly at page 40, lines 16-27 and page 41, line 24 to page 42, line 6. Claims 55 and 61 therefore add no new matter.

Applicants respectfully submit that the amendments and remarks herein place the present claims in condition for allowance, and earnestly solicit the same. Applicants invite the Examiner to call the undersigned

attorney of record if the Examiner believes that any remaining matters might be resolved more expeditiously by means of a telephonic interview.

Respectfully submitted,

6 Nov 2002

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Marked Up Version of the Amendment to the Specification Pursuant to 37 CFR § 1.121(b)(1)(iii)

Poly(A)+ mRNA was isolated from spleen and lymph nodes of unimmunized and immunized XenoMice using a Fast-Track kit (Invitrogen). The generation of random primed cDNA was followed by PCR. Human VH or human Vk family specific variable region primers (Marks et. al., 1991) or a universal human VH primer, MG-30 (CAGGTGCAGCTGGAGCAGTCIGG) (SEQ ID NO:11) was used in conjunction with primers specific for the human Cm (hmP2) or Ck (hkP2) constant regions as previously described (Green et al., 1994), or the human g2 constant region MG-40d; 5'-GCTGAGGGAGTAGAGTCCTGAGGA-3' (SEQ ID NO:12). PCR products were cloned into pCRII using a TA cloning kit (Invitrogen) and both strands were sequenced using Prism dye-terminator sequencing kits and an ABI 377 sequencing machine. Sequences of human Mabs-derived heavy and kappa chain transcripts were obtained by direct sequencing of PCR products generated from poly(A+) RNA using the primers described above. All sequences were analyzed by alignments to the "V BASE sequence directory" (Tomlinson et al., MRC Centre for Protein Engineering, Cambridge, UK) using MacVector and Geneworks software programs.